

Serial Number: 09/446,415C**ENTERED****RECEIVED**

MAY 22 2003

TECH CENTER 1600/2900

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☒ Inserted mandatory headings, specifically: 62207 (Seq 2)
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____



1600

RAW SEQUENCE LISTING

DATE: 05/15/2003

PATENT APPLICATION: US/09/446,415C

TIME: 20:01:38

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\05152003\I446415C.raw

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MAY 22 2003
TECH CENTER 1600/2900

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3 <110> APPLICANT: Beamer, Lesa J.
4     Eisenberg, David
5     Carroll, Stephen F.
7 <120> TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN
8     CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL
9     STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND
10    MOLECULAR MODELING OF RELATED PROTEINS
12 <130> FILE REFERENCE: 11034US02
14 <140> CURRENT APPLICATION NUMBER: 09/446,415C
15 <141> CURRENT FILING DATE: 2000-07-19
17 <150> PRIOR APPLICATION NUMBER: 08/879,565
18 <151> PRIOR FILING DATE: 1997-06-20
20 <160> NUMBER OF SEQ ID NOS: 14
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1813
26 <212> TYPE: DNA
27 <213> ORGANISM: Human
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31 <222> LOCATION: (31)..(1491)
33 <220> FEATURE:
34 <221> NAME/KEY: mat_peptide
35 <222> LOCATION: (124)..(1491)
37 <220> FEATURE:
38 <223> OTHER INFORMATION: "rBPI"
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41 caggccttga gggttttgga gctctggagg atg aga gag aac atg gcc agg ggc 54
42                               Met Arg Glu Asn Met Ala Arg Gly
43                               -30                -25
45 cct tgc aac gcg ccg aga tgg gtg tcc ctg atg gtg ctc gtc gcc ata 102
46 Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile
47       -20                -15                -10
49 ggc acc gcc gtg aca gcg gcc gtc aac cct ggc gtc gtg gtc agg atc 150
50 Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile
51       -5                -1    1                5
53 tcc cag aag ggc ctg gac tac gcc agc cag cag ggg acg gcc gct ctg 198
54 Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu
55 10       15                20                25
57 cag aag gag ctg aag agg atc aag att cct gac tac tca gac agc ttg 246
58 Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe
59       30                35                40
61 aag atc aag cat ctt ggg aag ggg cat tat agc ttc tac agc atg gac 294

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62 Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp
63          45          50          55
65 atc cgt gaa ttc cag ctt ccc agt tcc cag ata agc atg gtg ccc aat 342
66 Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn
67          60          65          70
69 gtg ggc ctt aag ttc tcc atc agc aac gcc aat atc aag atc agc ggg 390
70 Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly
71          75          80          85
73 aaa tgg aag gca caa aag aga ttc tta aaa atg agc ggc aat ttt gac 438
74 Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp
75 90          95          100          105
77 ctg agc ata gaa ggc atg tcc att tcc gct gat ctg aag ctg ggc agt 486
78 Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser
79          110          115          120
81 aac ccc acg tca ggc aag ccc acc atc acc tgc tcc agc tgc agc agc 534
82 Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser
83          125          130          135
85 cac atc aac agt gtc cac gtg cac atc tca aag agc aaa gtc ggg tgg 582
86 His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp
87          140          145          150
89 ctg atc caa ctc ttc cac aaa aaa att gag tct gcg ctt cga aac aag 630
90 Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys
91          155          160          165
93 atg aac agc cag gtc tgc gag aaa gtg acc aat tct gta tcc tcc aag 678
94 Met Asn Ser Gln Val Cys Glu Lys Val Thr Asn Ser Val Ser Ser Lys
95 170          175          180          185
97 ctg caa cct tat ttc cag act ctg cca gta atg acc aaa ata gat tct 726
98 Leu Gln Pro Tyr Phe Gln Thr Leu Pro Val Met Thr Lys Ile Asp Ser
99          190          195          200
101 gtg gct gga atc aac tat ggt ctg gtg gca cct cca gca acc acg gct 774
102 Val Ala Gly Ile Asn Tyr Gly Leu Val Ala Pro Pro Ala Thr Thr Ala
103          205          210          215
105 gag acc ctg gat gta cag atg aag ggg gag ttt tac agt gag aac cac 822
106 Glu Thr Leu Asp Val Gln Met Lys Gly Glu Phe Tyr Ser Glu Asn His
107          220          225          230
109 cac aat cca cct ccc ttt gct cca cca gtg atg gag ttt ccc gct gcc 870
110 His Asn Pro Pro Pro Phe Ala Pro Pro Val Met Glu Phe Pro Ala Ala
111          235          240          245
113 cat gac cgc atg gta tac ctg ggc ctc tca gac tac ttc ttc aac aca 918
114 His Asp Arg Met Val Tyr Leu Gly Leu Ser Asp Tyr Phe Phe Asn Thr
115 250          255          260          265
117 gcc ggg ctt gta tac caa gag gct ggg gtc ttg aag atg acc ctt aga 966
118 Ala Gly Leu Val Tyr Gln Glu Ala Gly Val Leu Lys Met Thr Leu Arg
119          270          275          280
121 gat gac atg att cca aag gag tcc aaa ttt cga ctg aca acc aag ttc 1014
122 Asp Asp Met Ile Pro Lys Glu Ser Lys Phe Arg Leu Thr Thr Lys Phe
123          285          290          295
125 ttt gga acc ttc cta cct gag gtg gcc aag aag ttt ccc aac atg aag 1062
126 Phe Gly Thr Phe Leu Pro Glu Val Ala Lys Lys Phe Pro Asn Met Lys

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127          300          305          310
129 ata cag atc cat gtc tca gcc tcc acc ccg cca cac ctg tct gtg cag 1110
130 Ile Gln Ile His Val Ser Ala Ser Thr Pro Pro His Leu Ser Val Gln
131          315          320          325
133 ccc acc ggc ctt acc ttc tac cct gcc gtg gat gtc cag gcc ttt gcc 1158
134 Pro Thr Gly Leu Thr Phe Tyr Pro Ala Val Asp Val Gln Ala Phe Ala
135 330          335          340          345
137 gtc ctc ccc aac tcc tcc ctg gct tcc ctc ttc ctg att ggc atg cac 1206
138 Val Leu Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His
139          350          355          360
141 aca act ggt tcc atg gag gtc agc gcc gag tcc aac agg ctt gtt gga 1254
142 Thr Thr Gly Ser Met Glu Val Ser Ala Glu Ser Asn Arg Leu Val Gly
143          365          370          375
145 gag ctc aag ctg gat agg ctg ctc ctg gaa ctg aag cac tca aat att 1302
146 Glu Leu Lys Leu Asp Arg Leu Leu Glu Leu Lys His Ser Asn Ile
147          380          385          390
149 ggc ccc ttc ccg gtt gaa ttg ctg cag gat atc atg aac tac att gta 1350
150 Gly Pro Phe Pro Val Glu Leu Leu Gln Asp Ile Met Asn Tyr Ile Val
151          395          400          405
153 ccc att ctt gtg ctg ccc agg gtt aac gag aaa cta cag aaa ggc ttc 1398
154 Pro Ile Leu Val Leu Pro Arg Val Asn Glu Lys Leu Gln Lys Gly Phe
155 410          415          420          425
157 cct ctc ccg acg ccg gcc aga gtc cag ctc tac aac gta gtg ctt cag 1446
158 Pro Leu Pro Thr Pro Ala Arg Val Gln Leu Tyr Asn Val Val Leu Gln
159          430          435          440
161 cct cac cag aac ttc ctg ctg ttc ggt gca gac gtt gtc tat aaa 1491
162 Pro His Gln Asn Phe Leu Leu Phe Gly Ala Asp Val Val Tyr Lys
163          445          450          455
165 tgaaggcacc aggggtgccg ggggctgtca gccgcacctg ttcctgatgg gctgtggggc 1551
167 accggctgcc tttccccagg gaatcctctc cagatcttaa ccaagagccc cttgcaaact 1611
169 tcttcgactc agattcagaa atgatctaaa cacgaggaaa cattattcat tggaaaagt 1671
171 catggtgtgt atttttaggga ttatgagctt ctttcaaggg ctaaggctgc agagatattt 1731
173 cctccaggaa tcgtgtttca attgtaacca agaaatttcc atttgctgtt catgaaaaaa 1791
175 aacttctggt ttttttcatg tg 1813
178 <210> SEQ ID NO: 2
179 <211> LENGTH: 487
180 <212> TYPE: PRT
181 <213> ORGANISM: Human
183 <220> FEATURE:
184 <223> OTHER INFORMATION: "rBPI"
186 <400> SEQUENCE: 2
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188 -30 -25 -20
190 Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val
191 -15 -10 -5 -1 1
193 Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala
194 5 10 15
196 Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys
197 20 25 30

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199 Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly
200      35                      40                      45
202 His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser
203      50                      55                      60                      65
205 Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser
206                      70                      75                      80
208 Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe
209                      85                      90                      95
211 Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile
212                      100                     105                     110
214 Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr
215                      115                     120                     125
217 Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His
218      130                      135                      140                      145
220 Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
221                      150                      155                      160
223 Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys
224                      165                      170                      175
226 Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu
227                      180                      185                      190
229 Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu
230                      195                      200                      205
232 Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys
233      210                      215                      220                      225
235 Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro
236                      230                      235                      240
238 Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly
239                      245                      250                      255
241 Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala
242                      260                      265                      270
244 Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser
245                      275                      280                      285
247 Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val
248      290                      295                      300                      305
250 Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
251                      310                      315                      320
253 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
254                      325                      330                      335
256 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
257                      340                      345                      350
259 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
260                      355                      360                      365
262 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
263      370                      375                      380                      385
265 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
266                      390                      395                      400
268 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
269                      405                      410                      415
271 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val

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Input Set : A:\PTO.AMC.txt

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272          420          425          430
274 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe
275          435          440          445
277 Gly Ala Asp Val Val Tyr Lys
278 450          455
282 <210> SEQ ID NO: 3
283 <211> LENGTH: 456
284 <212> TYPE: PRT
285 <213> ORGANISM: Human
287 <220> FEATURE:
288 <223> OTHER INFORMATION: bactericidal/permeability-increasing protein (BPI)
289      (Figure 5)
291 <400> SEQUENCE: 3
292 Val Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr
293 1          5          10          15
295 Ala Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile
296          20          25          30
298 Lys Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys
299          35          40          45
301 Gly His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro
302          50          55          60
304 Ser Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile
305 65          70          75          80
307 Ser Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg
308          85          90          95
310 Phe Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser
311          100          105          110
313 Ile Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro
314          115          120          125
316 Thr Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val
317          130          135          140
319 His Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys
320 145          150          155          160
322 Lys Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu
323          165          170          175
325 Lys Val Thr Asn Ser Val Ser Ser Glu Leu Gln Pro Tyr Phe Gln Thr
326          180          185          190
328 Leu Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly
329          195          200          205
331 Leu Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met
332          210          215          220
334 Lys Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala
335 225          230          235          240
337 Pro Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu
338          245          250          255
340 Gly Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu
341          260          265          270
343 Ala Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu
344          275          280          285

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/446,415C

DATE: 05/15/2003

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1600

RAW SEQUENCE LISTING

DATE: 05/15/2003

PATENT APPLICATION: US/09/446,415C

TIME: 12:43:10

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Output Set: N:\CRF4\05152003\I446415C.raw

3 <110> APPLICANT: Beamer, Lesa J.
 4 Eisenberg, David
 5 Carroll, Stephen F.
 7 <120> TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN:
 8 CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL
 9 STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND
 10 MOLECULAR MODELING OF RELATED PROTEINS
 12 <130> FILE REFERENCE: 11034US02
 14 <140> CURRENT APPLICATION NUMBER: 09/446,415C
 15 <141> CURRENT FILING DATE: 2000-07-19
 17 <150> PRIOR APPLICATION NUMBER: 08/879,565
 18 <151> PRIOR FILING DATE: 1997-06-20
 20 <160> NUMBER OF SEQ ID NOS: 14
 22 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

178 <210> SEQ ID NO: 2

179 <211> LENGTH: 487

180 <212> TYPE: PRT

181 <213> ORGANISM: Human

182 <223> OTHER INFORMATION: "rBPI"

Does Not Comply
Corrected Diskette Needed

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 186 -30 -25 -20
 188 Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val
 189 -15 -10 -5 -1 1
 191 Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala
 192 5 10 15
 194 Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys
 195 20 25 30
 197 Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly
 198 35 40 45
 200 His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser
 201 50 55 60 65
 203 Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser
 204 70 75 80
 206 Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe
 207 85 90 95
 209 Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile
 210 100 105 110
 212 Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr

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Input Set : A:\11034US02 1-29-03.SEQ.txt

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213      115      120      125
215 Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His
216 130      135      140      145
218 Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
219      150      155      160
221 Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys
222      165      170      175
224 Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu
225      180      185      190
227 Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu
228      195      200      205
230 Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys
231 210      215      220      225
233 Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro
234      230      235      240
236 Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly
237      245      250      255
239 Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala
240      260      265      270
242 Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser
243      275      280      285
245 Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val
246 290      295      300      305
248 Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
249      310      315      320
251 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
252      325      330      335
254 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
255      340      345      350
257 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
258      355      360      365
260 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
261 370      375      380      385
263 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
264      390      395      400
266 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
267      405      410      415
269 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val
270      420      425      430
272 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe
273      435      440      445
275 Gly Ala Asp Val Val Tyr Lys
276 450      455

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DATE: 05/15/2003

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TIME: 12:43:11

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